Amendments to the Specification:

Please add the following new paragraph, on page 12, line 7:

Figure 11. Expression of CLASP-2 upon T-cell activation as assayed by Northern analysis. Jurkat cells were activated using PMA, lonomycin, and αCD28. RNA was prepared from cell culture aliquots at 0, 1, 2, 4, 8, 14 hours post activation and Northern analysis was performed (A). Hybridization signals obtained with a CLASP-2-specific probe were quantified using a phosphor imager system. Relative signal intensities (refers to total signal of the specific probe used) are shown in the bar diagram (B). The ethidium staining of the Northern gel (A) demonstrates even RNA loading.

Please amend the paragraph, on page 25, line 16 as follows:

5.2.1.1. Signal Peptide

The human CLASP-2 sequence presented in FIG. 1 encodes two potential start sites for translation. The first predicted methionine appears at nucleotide 278 (ATG). The second methionine appears at nucleotide 476. Both have an acceptable consensus sequence for a translational start (A/GxxATGG; Kozak, M., 1996, Mamm. Genome 7(8): 563-74). A polypeptide beginning at the second methionine is also predicted to encode a signal peptide capable of localizing the protein to the secretory pathway by SignalP, a signal sequence prediction program (Nielsen, H. *et al.*, 1997, Protein Eng. l0(1): 1-6). Polypeptides beginning at the first methionine are not predicted to contain a signal sequence; however, the consensus for signal prediction is only 80-90% accurate for known signal sequences. A third possibility for a translational start is that the cDNA listed in FIG. 1 is incomplete and another methionine is encoded in frame and upstream of the sequence shown in FIG.1. Further research demonstrated that third possibility was correct~~ and the full length sequences are presented in FIG. 11A~~.

Please amend the paragraphs beginning on page 45, line 1 (ending on page 46, line 2) as follows:

~~As shown in FIG 11 above,~~ [[t]]There are at least three CLASP-2 full length cDNA isoforms (A + Z, B + Z, and C + Z). Each of the isoforms uses a unique first exon (designated~~labelled~~ exon 1A (SEQ ID NO: 115, corresponding to -182 to -102), 1B (SEQ ID NO: 116, corresponding to -219 to -102), and 1C (SEQ ID NO: 117, corresponding to -143 to -102), followed by exon 2 and the rest of human CLASP2 DNA, shown in SEQ ID NO: 118, corresponding to -101 to 6690) (*see* ~~FIG. 11 and~~ Table 4 below).

Table 4: CLASP-2 Isoforms

CLASP-2 Isoform	~~FIG 11C~~ Schematic	Nucleotides
Isoform 1	A + Z	-182 to 6690
Isoform 2	B + Z	-219 to 6690
Isoform 3	C + Z	-143 to 6690

In one embodiment, the CLASP-2 polynucleotide has the sequence of ~~shown in FIG. 11~~ (Isoform 1, Isoform 2, or Isoform 3 as indicated in Table 4 above) or a fragment of these sequences ~~shown in FIG. 11~~ comprising at least about 1, 5, 10, 25 or 50 or more conti[[n]]guous nucleotides from nucleotides -182 to 1883 of Isoform 1, nucleotides -219 to 1883 of Isoform 2, or nucleotides -143 to 1883 of Isoform 3.

In another embodiment, CLASP-2 primers or probes comprise at least about 5, 10, 25 or 50 or more continguous nucleotides from nucleotides -182 to 1883 of Isoform 1, nucleotides -219 to 1883 of Isoform 2, or nucleotides -143 to 1883 of Isoform 3 as shown in Table 4~~FIG. 11 and~~ Table 4 above alone or in combination with SEQ ID NO: 1 or a fragment of SEQ ID NO:1.

In an aspect, the invention provides antibodies or binding fragments that bind the CLASP. In another embodiment, the invention provides antibodies that specifically bind to the

CLASP-2 isoforms in Table 4 ~~shown in FIG. 11~~ but not to the polypeptide encoded by SEQ ID NO: 1.

In one embodiment, the CLASP variants differ from those shown in FIG. 1 ~~or FIG. 11~~ (SEQ ID NOS 1, 3, 5, 7, 9, 115-118, etc[[.]]) by virtue of incorporating a different combination of exons than found in the exemplified sequences. For example, 81g01 (Genbank Accession Number AF85864; Locus HUMYN8lg0l; 526 bp; EST sequence submitted August 29, 1998 by Washington University at St. Louis; see FIG. 3A and FIG. 3B) is a variant of hCLASP-2 on the basis of CLASP-2 identity along certain stretches of the sequence. From 5' to 3', it begins with a 315 nucleotide stretch which is identical to CLASP-2A. It then has a gap relative to CLASP-2A that is identical to the GAP in another CLASP-2 isoform, hCLASP-2D (KIAA1058). In place of that gap, a 16 amino acid insert (48 nucleotides) is present which is not found in other isoforms, followed by another approximately 150 bp stretch of nucleotides once again identical to CLASP-2A. This is characteristic of an alternate splice due to the specific sequence identity on both sides of a differential stretch of nucleotides.

Please amend the paragraph beginning on page 47, line 1 as follows:

In various embodiments, CLASP-2 polynucleotide fragments include coding regions for, or regions hybridizable to, the CLASP-2 structural or functional domains described *supra*. As set out in the Figures, such preferred regions include the following domains/motifs: ITAM, DOCK, COILED/COILED, and PBM. Thus, for example, polypeptide fragments of CLASP-2 as shown in FIG. 1 and in Table 4~~FIG. 11~~[[-]](SEQ ID NO: 2, 4, 6, 10, 115, 116, 117, etc.,) falling within conserved domains are specifically contemplated by the present invention (see FIG. 3). Moreover, polynucleotide fragments encoding these domains are also contemplated. Such polypeptide fragments find use, for example, as inhibitors of CLASP-2 function in CLASP-2-expressing cells.

Please amend the paragraph on page 68, line 29 as follows:

As described above, upon sequencing of numerous independent cDNA products, single nucleotide polymorphisms (SNPs) have been discovered within CLASP-2. These alterations and differences are presented~~ in FIG 11B~~. They represent mis-sense alterations.

Please amend the paragraph beginning on page 112, line 29 as follows:

To obtain additional 5' CLASP-2 sequence, portions of the cDNA and genomic sequence from a BAC (Bacterial Artificial Chromosome) genomic library were compared to the NCBI database by BLAST. A genomic clone (Genbank identifier: gi9988160) comprising random, shotgun genomic sequence was identified. Using TFASTX (Pearson and Lipman, PNAS (1988) 85:2444-2448), the amino-terminal sequence of human CLASP4 was compared to 6 frame translation of gi9988160. Areas of gi9988160 that encoded amino acids with high similarity to CLASP4 amino acid sequence were used to design CLASP-2-specific oligonucleotides for RTPCR (reverse transcriptase polymerase chain reaction according to manufacturers instructions: Reverse transcriptase Gibco/BRL, Taq Polymerase from Sigma). Using oligonucleotides hC2gS5 (nucleotides -66 to -44 in Table 4~~ of FIG. 11~~) and C2AS18 (reverse complement of nucleotides 2120 to 2140 in Table 4~~ of FIG. 11~~) an RTPCR product of approximately 2.2kb was generated, sequenced (dideoxynucleotide termination sequencing, Beckman Coulter CEQ2000) and shown to be additional human CLASP-2 5' sequence. Further complicating the cloning full-length CLASP cDNA products was the difficulty to clone (and subclone) certain CLASP cDNA products. Standard isolation of some of the CLASP cDNAs from a pure phage population following screening of commercially available cDNA libraries ("ZAP-out" procedure, Stratagene) resulted in no bacterial colonies. Similarly, certain RT-PCR products could not be cloned into standard plasmid vectors. No colonies were isolated by cloning these fragments into vectors lacking promoters, reverse orientations, low copy vectors, or by growth at altered temperatures or levels of antibiotic for plasmid selection (examples: CLASP-7 - HC7gS6 to HC7gASl and HC7gS3 to HC7AS14; CLASP-4 - C4P2 to hC4ASTM and C4P2 to HC4AS3'; CLASP-1 - hC1S5' to hClAS3'Kpn and C1S7 to hClAS3'Kpn; see Primer Table

below). One possibility is that sequences contained within certain regions of CLASP cDNAs are bacteriacidal and therefore not amenable to cloning. To circumvent these problems direct sequencing of RT-PCR products was performed.

Please amend the paragraph beginning on page 114, line 17 as follows:

RACE was carried out using Generacer kit (Invitrogen) according to manufacturers specifications using polyA selected mRNA from 9D10 B cell tissue culture line. The sequence of the oligonucleotides presented is the reverse complement *(i.e.,* antisense) of the [[the]] CLASP1 cDNA at the indicated position based upon numbering in Table 4~~FIG. 11~~.

Please amend the paragraph beginning on page 115, line 1 as follows:

The full length cDNA (presented in Table 4~~FIG. 11)~~ is therefore a compilation of cDNA from cDNA libraries, RTPCR products and 5' RACE products. ~~The sequence of the CLASP-2 cDNA is shown in FIG. 11.~~

Please amend the paragraph beginning on page 125, line 4 as follows:

Results

CLASP-2 expression levels as determined by Northern analysis (FIG. 11[[4]]) slightly decrease at 1 hour post activation. The maximum decrease of approximately 36 % is seen at 2 hours post activation. Expression levels augment again at 4 hours post activation but do not attain the level that is seen before activation (0 hours). Intensities of CLASP-2-specific signals on the Northern blot were quantified by phosphor imager analysis. Rectangles were drawn around the areas of CLASP-2-specific signal and total quantity of signal was determined by the "volume report" mode; phosphor imager quantification results of two entirely independent experiments are shown in the diagram (green bars corresponds to Northern blot shown). The above result suggests, that transcriptional control of CLASP-2 expression and T-cell activation are functionally linked to each other.